

REMARKS

Applicants appreciate the notification that the request to establish a continued prosecution application has been accepted and that the petition to correct inventorship has been entered.

Petition to Correct Inventorship

Applicants understand that the Petition to Correct Inventorship has been entered. Applicants wish to know whether the Petition to Correct Inventorship has been granted.

Rejections Under 35 U.S.C. §102(e)

The Examiner rejected claims 10-16 under 35 U.S.C. §102(e) as allegedly anticipated by Tygai et al. (U.S. Patent No. 6,277,607).

According to the Examiner, claims 10-16 are anticipated by Tygai et al. because the term "flank" used in claims 10 and 16 permits the inclusion of primer binding or hybridizing regions to the polymorphic site. Applicants believe the commonly understood meaning of the term "flank" excludes the possibility that the primers bind or hybridize to the polymorphic site. However, to further clarify the claims, Applicants have amended claims 10 and 16 to specify that "two amplification primers that hybridize to both the first nucleic acid molecule and the second nucleic acid molecule at locations which flank the polymorphic site such that neither the first primer nor the second primer hybridizes to the polymorphic site". In view of the forgoing, Applicants respectfully request that the Examiner withdraw the rejections under 35 U.S.C. §102(e).

Applicant : Jeffrey Olson et al.
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Attorney's Docket No.: 11926-112001

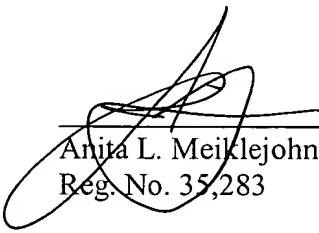
Conclusion

Attached is a marked-up version of the changes being made by the current amendment.

Applicant asks that all claims be allowed. Please apply any other charges or credits to
Deposit Account No. 06-1050.

Respectfully submitted,

Date: 12 NOV 02



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Version with markings to show changes made

In the claims:

Claims 10 and 16 have been amended as follows:

10. (Amended) A method for biasing a DNA amplification reaction such that a first nucleic acid molecule having a first nucleotide present at a polymorphic site is amplified to a greater extent than a second nucleic acid molecule having a second, different nucleotide present at the polymorphic site, comprising

(a) contacting a sample of DNA comprising at least the first nucleic acid molecule with two amplification primers that hybridize to both the first nucleic acid molecule and the second nucleic acid molecule at locations which flank the polymorphic site such that neither the first primer nor the second primer hybridizes to the polymorphic site, one of the two primers including a 5' portion which, when incorporated into an amplification product, will upon further amplification yield products that form a stable stem-loop structure, the stem of which is perfectly matched and includes the polymorphic site only when the second nucleotide is present at the polymorphic site, but not when the first nucleotide is present at the polymorphic site; and

(b) carrying out an amplification reaction, whereby the first nucleic acid molecule is amplified to a greater extent than the second nucleic acid molecule.

16. (amended) A method for haplotyping a first nucleic acid molecule having a first nucleotide present at a polymorphic site present in a sample of DNA comprising at least the first nucleic acid molecule and a second nucleic acid molecule having a second, different nucleotide present at the polymorphic site, comprising:

(a) contacting a sample of DNA comprising at least the first nucleic acid molecule with two amplification primers that hybridize to both the first nucleic acid molecule and the second nucleic acid molecule at locations which flank the polymorphic site such that neither the first primer nor the second primer hybridizes to the polymorphic site, one of the two primers

including a 5' portion which, when incorporated into an amplification product, will upon further amplification yield products that form a stable stem-loop structure, the stem of which is perfectly matched and includes the polymorphic site only when the second nucleotide is present at the polymorphic site, but not when the first nucleotide is present at the polymorphic site;

(b) carrying out an amplification reaction, whereby the first nucleic acid molecule is amplified to a greater extent than the second nucleic acid molecule to create an amplified DNA sample; and

(c) determining the nucleotide sequence of at least a portion of the DNA present in the amplified DNA sample.